

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 3, 2005, 01:56:21 ; Search time 4713 Seconds  
(without alignments)  
4318.097 Million cell updates/sec

Title: US-10-735-256-2  
Perfect score: 2226  
Sequence: 1 MLPGLRRLQLQAPASACLLLM.....LSAGLPSPLLCLLLLVPPhL 420

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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583

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4: gb\_om:\*  
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6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*

11: gb\_sts:\*  
 12: gb\_sy:\*  
 13: gb\_un:\*  
 14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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	1	2226	100.0 1260	6 AX411529	AX411529 Sequence
	2	2226	100.0 1263	6 AX751514	AX751514 Sequence
	3	2226	100.0 1263	9 AF532858	AF532858 Homo sapi
	4	2220	99.7 1263	9 AY250221	AY250221 Homo sapi
	5	2130	95.7 1263	6 AX751537	AX751537 Sequence
	6	2130	95.7 1304	10 AF532860	AF532860 Rattus no
	7	2118	95.1 1263	10 AY250220	AY250220 Mus muscu
	8	1866.5	83.8 1075	6 CQ728617	CQ728617 Sequence
	9	1342.5	60.3 143899	2 AC013606	AC013606 Homo sapi
	10	1342.5	60.3 143899	6 AX411543	AX411543 Sequence
	11	1342.5	60.3 165434	2 AC087505	AC087505 Homo sapi
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	13	1342.5	60.3 187566	2 AC015685	AC015685 Homo sapi
	14	1280	57.5 214711	2 AC108295	AC108295 Rattus no
c	15	1280	57.5 236864	2 AC096003	AC096003 Rattus no
	16	1272.5	57.2 196786	2 AC102636	AC102636 Mus muscu
c	17	1272.5	57.2 199873	10 AL928914	AL928914 Mouse DNA
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	20	977.5	43.9 1565	5 AY263332	AY263332 Danio rer
	21	966.5	43.4 163986	2 CR812832	CR812832 Danio rer
	22	951	42.7 180865	2 BX908740	BX908740 Danio rer
	23	951	42.7 198219	2 CR381666	CR381666 Danio rer
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	25	950	42.7 269285	2 AC120096	AC120096 Rattus no
	26	948	42.6 1326	9 AF532859	AF532859 Homo sapi
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c	29	948	42.6 166138	9 AC099684	AC099684 Homo sapi
	30	948	42.6 202269	9 AC130689	AC130689 Homo sapi
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	33	946	42.5 1509	10 AY311478	AY311478 Rattus no
	34	931.5	41.8 3509	5 AY263333	AY263333 Danio rer
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	42	837.5	37.6 1176	6 AX411541	AX411541 Sequence
	43	826	37.1 157732	2 AC099825	AC099825 Papio ham

AC092532 Papio anu  
AC007663 Homo sapi

## ALIGNMENTS

## RESULT 1

AX411529

LOCUS AX411529 1260 bp DNA linear PAT 14-JUN-2002

**DEFINITION** Sequence 1 from Patent WO0229059.

ACCESSION AX411529

VERSION AX411529.1 GI:21444134

## KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS Sah, D.W.Y., Cate, R.L. and Strittmatter, S.M.

TITLE        Nogo receptor homologs

JOURNAL Patent: WO 0229059-A 1 11-APR-2002;

BIOGEN INC (US)

## FEATURES

Location/Qualifiers

source

1. .1260

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/organism="Homo sapiens"
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/mol type="unassigned DNA"
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/db xref="taxon:9606"
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## ORIGIN

Alignment Scores:

Pred. No.:	1.89e-105	Length:	1260
Score:	2226.00	Matches:	420
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-735-256-2 (1-420) x AX411529 (1-1260)

Qy 1 MetLeuProGlyLeuArgArgLeuLeuGlnAlaProAlaSerAlaCysLeuLeuLeuMet 20

Db 1 ATGCTGCCCCGGGCTCAGGCGCCTGCTGCAAGCTCCCGCCTCGGCCTGCCTCCTGCTGATG 60

Qy 21 LeuLeuAlaLeuProLeuAlaAlaProSerCysProMetLeuCysThrCysTyrSerSer 40

Db 61 CTCCTGGCCCTGCCCCTGGCGGCCCCCAGCTGCCCCATGCTCTGCACCTGCTACTCATCC 120

Qy            41 ProProThrValSerCysGlnAlaAsnAsnPheSerSerValProLeuSerLeuProPro 60  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 121 CCGCCACCGTGAGCTGCCAGGCCAACAACTTCTCCTCTGTGCCGCTGTCCCTGCCACCC 180

Qy           61 SerThrGlnArgLeuPheLeuGlnAsnAsnLeuIleArgThrLeuArgProGlyThrPhe 80  
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Db 181 AGCACTCAGCGACTCTTCCTGCAGAACCTCATCCGCACGCTGCGGCCAGGCACCTTT 240

Qy.           81 GlySerAsnLeuLeuThrLeuTrpLeuPheSerAsnAsnLeuSerThrIleTyrProGly 100  
              | | | | | | | | | | | | | | | | | | | | | |

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 3, 2005, 01:05:36 ; Search time 619 Seconds  
(without alignments)  
4016.626 Million cell updates/sec

Title: US-10-735-256-2  
Perfect score: 2226  
Sequence: 1 MLPGLRRLQLQAPASACLLLM.....LSAGLPSPLLCLLLLVPPhL 420

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	2226	100.0	2182	10	ADF28509	Adf28509 NgRHy DNA	
5	2226	100.0	2182	13	ADS09832	Ads09832 Human the	
6	2186	98.2	1865	8	AAD51236	Aad51236 Human REM	
7	2181	98.0	1976	12	ADM72161	Adm72161 Human NTR	
8	2177	97.8	2565	10	ADE06964	Ade06964 Novel cod	
9	2130	95.7	1263	8	ACC70357	Acc70357 Nucleotid	
10	2127.5	95.6	2425	5	AAS79360	Aas79360 DNA encod	
11	2085	93.7	2499	10	ADF28508	Adf28508 NgRHy con	
12	1822.5	81.9	1598	10	ADC13558	Adc13558 Human NOV	
13	1342.5	60.3	143899	6	AAL38336	Aal38336 Genomic s	
14	1291	58.0	791	6	ABK34490	Abk34490 Human cDN	
15	1281	57.5	1003	2	AAX30364	Aax30364 DNA encod	
16	1281	57.5	1003	10	ADB47736	Adb47736 Novel hum	
17	1281	57.5	1003	12	ADJ55291	Adj55291 Novel hum	
18	948	42.6	1436	8	AAL55323	Aal55323 Human NgR	
19	948	42.6	1539	12	ADN12046	Adn12046 Novel hum	
20	946	42.5	1407	8	AAL55338	Aal55338 Rat NgRH2	
21	946	42.5	1480	12	ADN12048	Adn12048 Novel rat	
c 22	921	41.4	215980	6	AAL38337	Aal38337 Complemen	
23	920.5	41.4	1383	6	AAL38334	Aal38334 Mouse NgR	
24	842	37.8	972	5	AAS79358	Aas79358 DNA encod	
25	837.5	37.6	1176	6	AAL38335	Aal38335 Partial h	
26	818.5	36.8	1973	12	ADQ85992	Adq85992 Human tum	
27	816.5	36.7	1719	4	AAS09451	Aas09451 Human cDN	
28	816.5	36.7	1719	9	ACC81046	Acc81046 Human Nog	
29	816.5	36.7	2138	12	ADQ23729	Adq23729 Human sof	
30	816.5	36.7	2236	2	AAZ34229	Aaz34229 Human PRO	
31	816.5	36.7	2236	3	AAC58591	Aac58591 Human PRO	
32	816.5	36.7	2236	3	AAC78557	Aac78557 Human PRO	
33	816.5	36.7	2236	3	AAA77613	Aaa77613 Human PRO	
34	816.5	36.7	2236	3	AAA49724	Aaa49724 Human PRO	
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36	816.5	36.7	2236	5	AAC88958	Aac88958 Human PRO	
37	816.5	36.7	2236	5	AAC91467	Aac91467 Human PRO	
38	816.5	36.7	2236	8	ACA63797	Aca63797 Novel hum	
39	816.5	36.7	2236	8	ACA03793	Aca03793 cDNA enco	
40	816.5	36.7	2236	8	ACA71961	Aca71961 Human sec	
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42	816.5	36.7	2236	8	ABX92601	Abx92601 cDNA enco	
43	816.5	36.7	2236	8	ACD41985	Acd41985 Human sec	
44	816.5	36.7	2236	8	ACA66342	Aca66342 Human cDN	

## ALIGNMENTS

## RESULT 1

AAL38333

ID AAL38333 standard; cDNA; 1260 BP.

XX

AC AAL38333;

XX

DT 15-AUG-2002 (first entry)

XX

DE Human NgR2 cDNA sequence derived from genomic sequence AC013606.

XX

KW Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue;  
 KW NgR2; NgR3; axonal growth; central nervous system; CNS; cerebral injury;  
 KW spinal cord injury; stroke; demyelinating disease; multiple sclerosis;  
 KW monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease;  
 KW multifocal leukoencephalopathy; panencephalitis; Spongy degeneration;  
 KW Alexander's disease; Canavan's disease; metachromatic leukodystrophy;  
 KW Krabbe's disease; immune; bait protein; genetic mapping; gene therapy;  
 KW transgenic animal; unregulated cellular growth; cancer; tumour; human;  
 KW gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS

1. .1260

FT

/\*tag= a

FT

/product= "Protein of human NgR2"

FT

/note= "No stop codon"

FT

sig\_peptide

1. .90

FT

/\*tag= b

XX

PN WO200229059-A2.

XX

PD 11-APR-2002.

XX

PF 06-OCT-2001; 2001WO-US031488.

XX

PR 06-OCT-2000; 2000US-0238361P.

XX

PA (UYA ) UNIV YALE.

PA

(BIOJ ) BIOGEN INC.

XX

PI Strittmatter SM, Cate RL, Sah DWY;

XX

DR WPI; 2002-416677/44.

DR

P-PSDB; AAO21477.

XX

PT Novel Nogo receptor homolog polypeptide, NgR2 or NgR3, useful for  
 PT treating central nervous system disorder, cerebral injury, spinal cord  
 PT injury, stroke, and demyelinating diseases.

XX

PS Example 2; Page 103; 277pp; English.

XX

CC The invention relates to a Nogo receptor homologue polypeptide, NgR2 or  
 CC NgR3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid NTLRRCT  
 CC sequence, or a 420, 461 or 392 amino acid sequence, all given in the  
 CC specification. The NgR3 protein or its binding antibody is useful for  
 CC decreasing inhibition of axonal growth of a central nervous system (CNS)  
 CC neuron, by contacting the neuron NgR3 or its antibody, and for treating  
 CC CNS disease, disorder or injury. NgR3 or a vector comprising NgR3 is  
 CC useful for treating cerebral injury, spinal cord injury, stroke,  
 CC demyelinating diseases, e.g. multiple sclerosis, monophasic  
 CC demyelination, encephalomyelitis, multifocal leukoencephalopathy,  
 CC panencephalitis, Marchiafava-Bignami disease, Spongy degeneration,  
 CC Alexander's disease, Canavan's disease, metachromatic leukodystrophy and  
 CC Krabbe's disease. NgR3 is useful for inducing an immune response in a  
 CC mammal against NgR3, as a bait protein in a two-hybrid or three-hybrid  
 CC assay, and as a research tool for identification, characterisation and  
 CC purification of interacting, regulatory proteins. The nucleotide  
 CC sequences of the invention are useful for screening for RFLP associated  
 CC with certain disorders, for genetic mapping, and for gene therapy. The  
 CC vector containing NgR3 is useful for producing non-human transgenic  
 CC animals. The NgR3 binding antibody is useful for isolating and purifying  
 CC NgR3, for localisation and/or quantitation of NgR3, and for diagnostic  
 CC and therapeutic purposes. The sequences of the invention, vectors and  
 CC antibodies are useful for treating or preventing unregulated cellular  
 CC growth such as cancer and tumour growth. This polynucleotide sequence  
 CC represents the human NgR2 cDNA sequence derived from the genomic sequence  
 CC AC013606 of the invention

XX

SQ Sequence 1260 BP; 170 A; 524 C; 364 G; 202 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.84e-129	Length:	1260
Score:	2226.00	Matches:	420
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-735-256-2 (1-420) x AAL38333 (1-1260)

Qy	1 MetLeuProGlyLeuArgArgLeuLeuGlnAlaProAlaSerAlaCysLeuLeuLeuMet	20
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Qy	21 LeuLeuAlaLeuProLeuAlaAlaProSerCysProMetLeuCysThrCysTyrSerSer	40
Db	61 CTCCTGGCCCTGCCCTGGCGCCCCCAGCTGCCCCATGCTCTGCACCTGCTACTCATCC	120
Qy	41 ProProThrValSerCysGlnAlaAsnAsnPheSerSerValProLeuSerLeuProPro	60
Db	121 CCGCCACCGTGAGCTGCCAGGCCAACAACTTCTCCTCTGTGCGCTGTCCCTGCCACCC	180
Qy	61 SerThrGlnArgLeuPheLeuGlnAsnAsnLeuIleArgThrLeuArgProGlyThrPhe	80
Db	181 AGCACTCAGCGACTCTTCTGCGAACAACCTCATCCGACGCTGCGGCCAGGCACCTTT	240
Qy	81 GlySerAsnLeuLeuThrLeuTrpLeuPheSerAsnAsnLeuSerThrIleTyrProGly	100

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 3, 2005, 02:31:26 ; Search time 223 Seconds  
(without alignments)  
3081.777 Million cell updates/sec

Title: US-10-735-256-2  
Perfect score: 2226  
Sequence: 1 MLPGLRRLQLQAPASACLLLM.....LSAGLPSPLLCLLLLVPPhL 420

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 ; Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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583

-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4:	/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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6:	/cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1281	57.5	1003	4	US-09-774-639-58	Sequence 58, Appl
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3	816.5	36.7	1422	4	US-09-949-016-2577	Sequence 2577, Ap
4	800.5	36.0	1777	4	US-09-461-325-40	Sequence 40, Appl
5	800.5	36.0	1777	4	US-10-012-542-40	Sequence 40, Appl
6	800.5	36.0	1777	4	US-10-115-123-40	Sequence 40, Appl
7	393.5	17.7	2713	4	US-09-949-016-2833	Sequence 2833, Ap
8	388.5	17.5	32278	4	US-09-949-016-14575	Sequence 14575, A
9	380.5	17.1	2852	3	US-09-063-950-1	Sequence 1, Appli
10	377.5	17.0	9036	4	US-09-949-016-16866	Sequence 16866, A
11	374.5	16.8	2587	4	US-09-949-016-5124	Sequence 5124, Ap
12	370.5	16.6	2019	3	US-09-063-950-3	Sequence 3, Appli
13	338	15.2	2341	4	US-09-520-781-9	Sequence 9, Appli
14	338	15.2	2607	4	US-09-520-781-11	Sequence 11, Appl
15	337.5	15.2	2906	4	US-09-907-794A-291	Sequence 291, App
16	337.5	15.2	2906	4	US-09-905-125A-291	Sequence 291, App
17	337.5	15.2	2906	4	US-09-902-775A-291	Sequence 291, App
18	337.5	15.2	2906	4	US-09-906-700-291	Sequence 291, App
19	337.5	15.2	2906	4	US-09-903-603A-291	Sequence 291, App
20	337.5	15.2	2906	4	US-09-904-920A-291	Sequence 291, App
21	337.5	15.2	2906	4	US-09-909-064-291	Sequence 291, App
22	337.5	15.2	2906	4	US-09-905-381A-291	Sequence 291, App
23	337.5	15.2	2906	4	US-09-906-618-291	Sequence 291, App
24	334	15.0	1356	4	US-09-520-781-31	Sequence 31, Appl
25	331	14.9	8378	5	PCT-US91-09055-1	Sequence 1, Appli
26	330.5	14.8	3679	4	US-09-907-794A-244	Sequence 244, App
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28	330.5	14.8	3679	4	US-09-902-775A-244	Sequence 244, App
29	330.5	14.8	3679	4	US-09-906-700-244	Sequence 244, App
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33	330.5	14.8	3679	4	US-09-905-381A-244	Sequence 244, App
34	330.5	14.8	3679	4	US-09-906-618-244	Sequence 244, App
35	328.5	14.8	2290	4	US-09-907-794A-72	Sequence 72, Appl
36	328.5	14.8	2290	4	US-09-905-125A-72	Sequence 72, Appl
37	328.5	14.8	2290	4	US-09-902-775A-72	Sequence 72, Appl
38	328.5	14.8	2290	4	US-09-906-700-72	Sequence 72, Appl
39	328.5	14.8	2290	4	US-09-903-603A-72	Sequence 72, Appl
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44	328	14.7	7452	3	US-08-592-500-1	Sequence 1, Appli
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## ALIGNMENTS

RESULT 1  
US-09-774-639-58

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; Sequence 58, Application US/09774639
; Patent No. 6806351
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 1003
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (422)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (700)
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; NAME/KEY: SITE
; LOCATION: (758)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-774-639-58
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Alignment Scores:

Pred. No.:	4.26e-108	Length:	1003
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DB:	4	Gaps:	0

US-10-735-256-2 (1-420) x US-09-774-639-58 (1-1003)

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Qy      21 LeuLeuAlaLeuProLeuAlaAlaProSerCysProMetLeuCysThrCysTyrSerSer 40
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Qy      60 oSerThrGlnArgLeuPheLeuGlnAsnAsnLeuIleArgThrLeuArgProGlyThrPh 80
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Qy      80 eGlySerAsnLeuLeuThrLeuTrpLeuPheSerAsnAsnLeuSerThrIleTyrProGl 100
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 3, 2005, 02:41:31 ; Search time 728 Seconds  
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3778.219 Million cell updates/sec

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Perfect score: 2226  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7338684 seqs, 3274456166 residues

Total number of hits satisfying chosen parameters: 14677368

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	2226	100.0	1260	10	US-09-972-546-1	Sequence 1, Appli
2	2226	100.0	1260	21	US-10-735-256-1	Sequence 1, Appli
3	2186	98.2	1865	21	US-10-477-714-43	Sequence 43, Appl
4	1822.5	81.9	1598	17	US-10-188-248-37	Sequence 37, Appl
5	1342.5	60.3	143899	10	US-09-972-546-15	Sequence 15, Appl
6	1342.5	60.3	143899	21	US-10-735-256-15	Sequence 15, Appl
7	1291	58.0	791	9	US-09-823-245A-259	Sequence 259, App
8	1281	57.5	1003	10	US-09-774-639-58	Sequence 58, Appl
9	1281	57.5	1003	10	US-09-969-730-19	Sequence 19, Appl
10	1281	57.5	1003	17	US-10-621-363-19	Sequence 19, Appl
11	948	42.6	1436	20	US-10-487-886-1	Sequence 1, Appli
12	946	42.5	1407	20	US-10-487-886-24	Sequence 24, Appl
c 13	921	41.4	215980	10	US-09-972-546-16	Sequence 16, Appl
c 14	921	41.4	215980	21	US-10-735-256-16	Sequence 16, Appl
15	920.5	41.4	1383	10	US-09-972-546-3	Sequence 3, Appli
16	920.5	41.4	1383	21	US-10-735-256-3	Sequence 3, Appli
17	837.5	37.6	1176	10	US-09-972-546-13	Sequence 13, Appl
18	837.5	37.6	1176	21	US-10-735-256-13	Sequence 13, Appl
19	816.5	36.7	1719	9	US-09-758-140-1	Sequence 1, Appli
20	816.5	36.7	1719	9	US-09-972-599A-1	Sequence 1, Appli
21	816.5	36.7	2138	20	US-10-723-860-6549	Sequence 6549, Ap
22	816.5	36.7	2236	9	US-09-978-295A-399	Sequence 399, App
23	816.5	36.7	2236	9	US-09-978-697-399	Sequence 399, App
24	816.5	36.7	2236	9	US-09-978-192A-399	Sequence 399, App
25	816.5	36.7	2236	9	US-09-999-832A-399	Sequence 399, App
26	816.5	36.7	2236	10	US-09-978-189-399	Sequence 399, App
27	816.5	36.7	2236	10	US-09-978-608A-399	Sequence 399, App
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Qy	81	GlySerAsnLeuLeuThrLeuTrpLeuPheSerAsnAsnLeuSerThrIleTyrProGly	100
Db	241	GGGTCCAACCTGCTCACCTGTGGCTCTTCTCAACAACCTCTCCACCATCTACCCGGGC	300
Qy	101	ThrPheArgHisLeuGlnAlaLeuGluGluLeuAspLeuGlyAspAsnArgHisLeuArg	120
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Db	361	TCGCTGGAGCCCGACACCTTCCAGGGCCTGGAGCGGCTGCAGTCGCTGCATTTGTACCGC	420
Qy	141	CysGlnLeuSerSerLeuProGlyAsnIlePheArgGlyLeuValSerLeuGlnTyrLeu	160
Db	421	TGCCAGCTCAGCAGCCTGCCCAGCAACATCTTCCGAGGCCTGGTCAGCCTGCAGTACCTC	480
Qy	161	TyrLeuGlnGluAsnSerLeuLeuHisLeuGlnAspAspLeuPheAlaAspLeuAlaAsn	180
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Qy	201	GlyLeuGlySerLeuAspArgLeuLeuLeuHisGlyAsnArgLeuGlnGlyValHisArg	220
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Qy	261	AsnProTrpAlaCysAspCysArgAlaArgProLeuTrpAlaTrpPheGlnArgAlaArg	280
Db	781	AACCCCTGGGCGTGCGACTGCCGCGCGCGGCCGCTCTGGGCCTGGTTCCAGCGCGCGCGC	840
Qy	281	ValSerSerSerAspValThrCysAlaThrProProGluArgGlnGlyArgAspLeuArg	300
Db	841	GTGTCCAGCTCCGACGTGACCTGCGCCACCCCCCGAGCGCCAGGGCCGAGACCTGCGC	900
Qy	301	AlaLeuArgGluAlaAspPheGlnAlaCysProProAlaAlaProThrArgProGlySer	320
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Qy      361 GlyGlyAspAlaProThrGluAspAspTyrTrpGlyGlyTyrGlyGlyGluAspGlnArg 380
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Db     1081 GGCGGGGACGCGCCTACTGAGGACGACTACTGGGGGGGCTACGGGGGTGAGGACCAGCGA 1140

Qy      381 GlyGluGlnMetCysProGlyAlaAlaCysGlnAlaProProAspSerArgGlyProAla 400
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Db     1141 GGGGAGCAGATGTGCCCCGGCGCTGCCTGCCAGGCGCCCCCGGACTCCCCAGGCCCTGCG 1200

Qy      401 LeuSerAlaGlyLeuProSerProLeuLeuCysLeuLeuLeuValProHisHisLeu 420
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# RESULT 2

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US-10-735-256-1
; Sequence 1, Application US/10735256
; Publication No. US20050048520A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; APPLICANT: CATE, RICHARD L.
; APPLICANT: SAH, DINAH W.Y.
; TITLE OF INVENTION: NOGO RECEPTOR HOMOLOGS
; FILE REFERENCE: A116 CON
; CURRENT APPLICATION NUMBER: US/10/735,256
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/972,546
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 60/238,361
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-735-256-1

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US-10-735-256-2 (1-420) x US-10-735-256-1 (1-1260)

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 3, 2005, 02:00:16 ; Search time 3358 Seconds  
(without alignments)  
4760.868 Million cell updates/sec

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Perfect score: 2226  
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Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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9: gb\_gss2:\*



Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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	6	916	41.2	2442	3	AK033286 Mus muscu
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	17	817	36.7	1639	3	CR595137 full-leng
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	20	816.5	36.7	1911	3	CR620900 full-leng
	21	776	34.9	501	8	AQ939452 NR1-154R
	22	758	34.1	1146	3	CR590252 full-leng
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	32	688	30.9	930	4	BI760526 603045070
	33	684	30.7	1302	4	BM807465 AGENCOURT
	34	673	30.2	385	6	CB702344 AMGNNUC:S
	35	673	30.2	771	4	BG469747 602534219
c	36	661.5	29.7	415	2	AW131579 xf31f08.x
	37	659	29.6	367	2	BF940539 nae21h02.
c	38	654	29.4	384	2	AW293195 UI-H-BI2-
	39	652	29.3	907	5	BU540705 AGENCOURT
	40	648	29.1	884	5	BX331981 BX331981
	41	643.5	28.9	1052	5	BX461669 BX461669
	42	640.5	28.8	953	5	BU500558 AGENCOURT
	43	634	28.5	675	7	CK961565 4075847 B
	44	594	26.7	544	6	CB612057 AMGNNUC:N
c	45	591	26.5	1018	5	BX388350 BX388350

# ALIGNMENTS

RESULT 1

BU707423

LOCUS BU707423 751 bp mRNA linear EST 15-JUL-2003

DEFINITION UI-M-FR0-cap-e-04-0-UI.r1 NIH\_BMAP\_FR0 Mus musculus cDNA clone  
IMAGE:6415467 5', mRNA sequence.

ACCESSION BU707423

VERSION BU707423.1 GI:23638879

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 751)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

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Tissue Procurement: Dr. Jim Lin, University of Iowa

cdna Library preparation: Dr. M. Bento Soares, University of Iowa

cdna Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

Seq primer: pYX-5.

FEATURES

source

Location/Qualifiers

1. .751

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6"

/db\_xref="taxon:10090"

/clone="IMAGE:6415467"

/tissue\_type="whole brain"

/dev\_stage="embryo 13.5,14.5,16.5,17.5dpc"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_lib="NIH\_BMAP\_FR0"

/note="Organ: Brain; Vector: pYX- Asc; Site\_1: EcoR I;

Site\_2: Not I; The library was constructed according

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction, ligated

with EcoR I adaptor, digested with NotI and then cloned  
directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail  
is AGCGAGACAG. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National

Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
program coordinator."

ORIGIN